

Aspergillus fumigatus NMT

1 ATGGCGAGTCGCTATTGGAAAAACACCCCGCTCTCAGGAACGAGACGGCGGCATGGACAAAAGACAGCGGCGGAGGCAATGGCAAAATGACATTG 100
M A E S L L E N N P A L R N E T A G M D K D K A A E A M R K M N I A

101 CCGAATTGCTGACAGGCTTGTCAGTTTCCGGGAAGAACCAGAAGGATATGGCTTCGTACAAGTTTGGCAACGCGAGCCTGTGCCCGGATTTCGATGAGAC 200
E L L T G L S V S G K N Q K D M A S Y K F W Q T Q P V P R F D E T

201 GAGTACCGATACTGGGGCCCTATCAAGATCATTTGATCCTGAAAGGTCTCAAGGAACCGGATGCGCTGTTGAAGGATTTGAATGGGCGACATCGAC 300
S T D T G G P I K I I D P E K V S K E P D A L L E G F E W A T L D

301 CTGACAAAACGAGACTGAGCTGCAGGAGCTGTGGGATTGTTGACGTATCACTACGTAGAGGACGACAATGCCATGTTCCGGTTCAGATATTGCGAGTCGT 400
L T N E T E L Q E L W D L L T Y H Y V E D N A M F R F R Y S Q S F

401 TCCTACACTGGGCTCTTATGTCGCTGGCTGGAAAAGGAATGGCATGTGCGGTGTCGCGCTACGAAGTCGCGCAACTGGTAGCGTCCATTGCGGTGT 500
L H W A L M S P G W K K E W H V G V R A T K S R K L V A S I C G V

501 CCGGACAGAGATCAATGTGGCAATCAAAAGCTCAAGGTCGTGAGATCAATTTCTCTGCATCCACAGAAGCTCCGCTCGAAGCGCTTGACCCCAAGTT 600
P T E I N V R N Q K L K V V E I N F L C I H K K L R S K R L T P V

601 CTCATCAAGAATAACCCGTCGTTGTACCTCAATGGCATCTACCAAGCCATCTACACTGGGGGTGTGGTGTCTCCCACTCTCTGTCTCAGCTCATGCCGCT 700
L I K E I T R R C Y L N G I Y Q A I Y T A G V V L P T P V S S C R Y

FIG. 1A

701	ACTACCACCGTCCTTTGGACTGGTTGAAGCTTTACGAGGTGGGTTCTCGCCTCTCCCTGCCGATCCACCAAGCGCGCCAGATCACCAAGAATCACCT Y H R P L D W L K L Y E V G F S P L P A G S T K A R Q I T K N H L	800
801	GCCCAGTACTACTCTACCCCGGTCTTCGCCCCCATGGAGCCCAAGACATTGACACAGTGCATGATCTTTGCAGCGATACTTGTGCGGTTTGCCTTG P S T T S T P G L R P M E P K D I D T V H D L L Q R Y L S R F A L	900
901	AACCGAGCCTTTACCGGAGAGGAAGTGGACCATTGGGCTCGTGCCACCAAGCGGAGACGGTCAAGAGAGCGTCGTCTGGGCATACGTGGTAGAGGACCCCTG N Q A F T R E E V D H W L V H K P E T V K E Q V V W A Y V V E D P E	1000
1001	AAACGACAAAGATACCGGACTCTCTTTCCCTTCTACAACCTCGAATCCACCGTCATTTCAGATCCCAAGCATGACAATGTGCGTGTCTTACCTGTACTA T H K I T D F F S F Y N L E S T V I Q N P K H D N V R A A Y L Y Y	1100
1101	CTATGCAACCGAAACAGCTTTCACCAATAACATGAAGGCTCTCAAGAGCGTCTGTGATGCTGATGAATGACGCTCTGATCCTGGCTAAGAAGCGGCAC Y A T E T A F T N N M K A L K E R L L M L M N D A L I L A K K A H	1200
1201	TTTGATGTGTTCAACGCACTTACGCTTCACGATAAACCCCTCTGTTCCTCGAACAACTCAAATTTTGAGCTGGCGATGGCAGCTTCACCTTCTACCTCTACA F D V F N A L T L H D N P L F L E Q L K F G A G D G Q L H F Y L Y N	1300
1301	ACTATCGCACCGCCCTGTCTCTGGAGGAGTTAACGAGAAGAACCTGCCGATGACAAAAGAATGGAGGCGTTGGCATCGTTATGCTGTAA Y R T A P V P G G V N E K N L P D E K R M G G V G I V M L *	1392

FIG. 1B

nm1 (Aspergillus fumigatus)

1	TCCGACTCTAAAGGATCGCAAGGCAAGGCCCCCGAGGCCAGTCTTCGAAAAAGAAAGATGGCGCGGTGAACATAACCCCTCAGATCGCGGAGTCGCTAT AGCGTGAGATTCTAGCGTTCCCGTTCGCGGGCTCCGGTCAGAAAGGTTTTCTTCTACCGGCCACTTGATTTGGGGAGTCTACCGCCTCAGCGATA	100
1	M A E S L L	6
101	TGGAAAAACAACCCCGCTCTCAGGAACGAGACGGCGCGCATGGAACAAGCAAGGGCGGAGGCAATCGCAAAATGAACATTTGCCGAATTGCTGACAGG ACCTTTTGTGGGGCGAGAGTCTTGCTCTGCGCGCGGTACCTGTTCTGTTCCGCGCGCTCCGTTACGCGTTTTACTTGTAAAGGCTTAACGACTGTCC	200
7	E N N P A L R N E T A G M D K D K A A E A M R K M N I A E L L T G	39
201	CTTGTCAAGTTTCCGGGAAGAACCAAGAGGATATGGCTTCGTACAAAGTTTGGCAAAACCGACCCGCTGTGCCACACGGGCTAAGCTACTCTGCTCATGGCTATGACCC GAACAGTCAAGGCCCTTCTTGCTCTCTATACGAAGCATGTTCAAAACCGTTTGGCTCGGACACGGGCTAAGCTACTCTGCTCATGGCTATGACCC	300
40	L S V S G K N Q K D M A S Y K F W Q T Q P V P R F D E T S T D T G	72
301	GGCCCTATCAAGATCATTTGATTCCTGAAGGTTCTCAAAGAAACCGATCGCTGTGAAGGATTTGAATGGCGGACACTCGACCTGACAAACGAGACTG CCGGATAGTTCTAGTAACCTAGGACTTTTTCAGAGTTTCTTGCCCTACGCGAGCACTTCTAAACTTACCCGCTGTGAGCTGGAAGTGTGCTCTGAC	400
73	G P I K I I D P E K V S K E P D A L L E G F E W A T L D L T N E T E	106
401	AGCTGCAGAGACTGTGGGATTTGTTGACGTATCACTACGTAGAGGACGACAAATGCCATGTTCCGGTTCAGATATTCGCAGTCGTTCCCTACACTGGTGGGT TCGACGTCCTCGACACCCCTAAACAACCTGCATAGTGCATCTCTCTGTTACGGTACAAGGCCAAGTCTATAAGCGTCACGAAGGATGTGACCAACCCA	500
107	L Q E L W D L L T Y H Y V E D D N A M F R F R Y S Q S F L H W	137
501	GCACAACGCGCCGAGGATCTGTTTCTACCGGCTTGGAGGTTGATTAATTGAGCGCTGACAAATTTTGACCGTAGGCTCTTATGTGCGCTGGCT CGTTTGGCGCGGCTCCCTAGACAAAGAGTGGCGGAACCCCTCCACACCTAATAAACTCGCGACTGTTAAACTGGCATCCCGAGATACAGCGGACCGA	600
	A L M S P G W	144
138		

FIG. 2A

601 GGAAAAGGAATCGCATGTCGGTCCGGCTACGAAGTCGCGCAAACTGGTAGCTCCATTTCGGGTGCCGACAGAGATCAATGTGCGCAATCAAAA
CCTTTTCTTACCGTACAGCCACAGCGCGGATGCTTCAGCGGCTTGAACCAATCGCAGGTAAACGCCACAGGCTGTCTCTAGTTACACGCGTTAGTTT
145 K K E W H V G V R A T K S R K L V A S I C G V P T E I N V R N Q K 177

701 GCTCAAGGTCGTGAGATCAATTTCTCTGATCCACAAAGAGCTCCGCTCGAAGGCTTGACCCCACTTCATCAAAAGAAATCACCCGTGCTGCTAC
CGAGTTCAGCAGCAGCTTAGTTAAAGAGACGTAGGTGTTCTTCGAGCGAGCTTCGCGAACTGGGTCAAGAGTAGTTCTTTAGTGGCAGCAACGATG
178 L K V V E I N F L C I H K K L R S K R L T P V L I K E I T R R C Y 210

801 CTCAATGGCATCTACCAAGCCATCTACACTGCGGTGTGGTCTCCCACTCTCTGTGAGCTCATGCCGCTTACCAACCGTCTTGGACTGTTGAAGC
GAGTTACCGTAGATGTTCCGTAGATGTGACGCCACACCGAGGGTGAGGACAGTCGAGTACGGCGATGATGGTGGCAGAAACCTGACCAACTTCG
211 L N G I Y Q A I Y T A G V V L P T P V S S C R Y Y H R P L D W L K L 244

901 TTTACGAGGTCGGCTTCTCGCTCTCCCTGCCGATCCACCAAGCGCGCAGATCACCAAGAAATCACCTGCCAGTACTACCTTACCCCGGTCTTCG
AAATGCTCCAGCCGAGAGCGGAGGAGCGGCTAGTGTGTTCCGGCGGTCTAGTGGTCTTAGTGGACGGGTCTGATGGAGATGGGCGCCAGAAAGC
245 Y E V G F S P L P A G S T K A R Q I T K N H L P S T T S T P G L R 277

1001 CCCCATGGAGCCCAAGACATTTGACACAGTGCATGATCTTTTGCAGCGATACTTGTCCGGTTCGCTTGAACCAAGGCTTTACGCGAGAGGAGTGGAC
GGGTACCTCGGGTTTCTGTAACTGTGTGTCAGTACTAGAAAACGTCGCTATGAACAGCGCCAAACGCAACTTGGTCCGAAATGCGCTCTCCTTCACCTG
278 P M E P K D I D T V H D L L Q R Y L S R F A L N Q A F T R E E V D 310

1101 CATTTGGCTGTGCACAAGCGGAGACGGTGAAGAGACAGTCTGTGGCATAGTGGTAGAGGACCCCTGAACGCCACAAGATCACCGACTTCTTTTCT
GTAACGAGCACGTGTTCCGCCCTCTGCCACTTTCGTCCAGCAGACCCGTATGCACCATCTCCTGGACTTTCGGTGTCTAGTGTGCTGAAGAAAGGA
311 H W L V H K P E T V K E Q V V W A Y V V E D P E T H K I T D F F S F 344

1201 TCTACAACCTCGAATCCACCGTCATTTCAGAAATCCCAAGCATGACAAATGTGCGTCTGCTTACTGTACTATGCAACCGAAACAGCTTTCACCAATAA
AGATGTTGGAGCTTAGGTGGCAGTAAGTCTTAGGTTTCGTACTGTTACACGACGACGAATGGACATGATGATACGTGGCTTGTGCAAGTGGTTATT
345 Y N L E S T V I Q N P K H D N V R A A Y L Y Y A T E T A F T N N 377

FIG. 2B

1301	CATGAAGCTCTCAAAGAGCGTCTGCTGATGCTGATGAATGACCGCTCTGATCTGGCTAAGAAGGTAACCTACAGGATCCACTGCCATTTCCTCGAGTTGTACTTCGGAGAGTTTCTCGCAGACGACTACGACTACTTACTCGGAGACTAGGACCGATTCTCCATTGATGTCCCTAGGTGACGGTAAGGGACCTCAA	1400
378	M K A L K E R L L M L M N D A L I L A K K A	399
1401	GACTTACGAAGCTTGACATTGTGTGATAGCGCACTTTGATGTTCAACCGCACTTACCGCTTACGATAACCCCTCTGTTCTCGAACAACTCAAAATTTGGCTGAATGCTTCGACTGTAAACACAACTATCCGGGTGAACTACACAAGTTGCGTGAATGCGAAGTCTATTGGGAGACAAGGAGCTTGTGAGTTTAAACC	1500
400	H F D V F N A L T L H D N P L F L E Q L K F G	422
1501	AGCTGGCGATGGGAGCTTCACTTCTACCTTACAACCTATCGCACCGCCCTGTTCTCGAGGAGTTAACGAGAAGAACCTGCCGGATGAGAAAAGAAATGTCGACCGCTACCCGTCGAAAGTGAAGATGGAGATGTTGATAGCGTGGCGGGGACAAGGACTCTCTCAATGCTTCTTGGACGGCTACTCTTTTCTTAC	1600
423	A G D G Q L H F Y L Y N Y R T A P V P G G V N E K N L P D E K R M	455
1601	GGAGCGTTGGCATCGTTATGCTGTAAAACAATCTCACCGCATGGACCAATGCCCTCTCGCCTCGTTGATGATCGCATCTTTATACCTATTTCTCGCTGTGACCCTCGCAACCGTAGCAATACGACATTTTGTGAAGAGTGGCGTACCTGGTACGGAGAGCGGAGCAACTACTAGCGTAGAATATGGATAAAGAGCGACACTG	1700
456	G G V G I V M L *	463
1701	ATGAATTTGGGTATGCGAAATACCATGAAATTTG TACTTAAACCCATACGCTTTTATGGTACTTTTAAAC	(SEQ ID NO:3) (SEQ ID NO:2)

FIG. 2C